

```

1  CGAGCCACGGCTTATGCAAGCAAGAATCTGGAGGAGCAGTTACGGTCTGTCCAGTGT
-----+-----+-----+-----+-----+-----+-----+
61 AGATGAAC TCA TGA C TGA C TCTAC CAGA TATTG GAA AATGTACAAGTGTCA GCTAAG
-----+-----+-----+-----+-----+-----+-----+
      M  T  V  L  Y  P  E  Y  W  K  M  Y  K  C  Q  L  R
-----+-----+-----+-----+-----+-----+-----+
121 GAAAGAGGCTGGCAACATAACAGAGAACAGGCCAACCTCACTCAAGGACAGAGAGAC
-----+-----+-----+-----+-----+-----+-----+
      K  G  G  W  Q  H  N  R  E  Q  A  N  L  N  S  R  T  E  E  T
-----+-----+-----+-----+-----+-----+-----+
181 TATATAAATTTCCTGCAGCACATTATAATACAGAGATCTTGAAAGTATTGATTAATGAGTG
-----+-----+-----+-----+-----+-----+-----+
      I  K  F  A  A  A  H  Y  N  T  E  I  L  K  S  I  D  N  E  W
-----+-----+-----+-----+-----+-----+-----+
241 GAGAAAGACTCAATGCATGCCACGGAGGTGTGTATAGATGTGGGAGAGAGTTTGAGT
-----+-----+-----+-----+-----+-----+-----+
      R  K  T  Q  C  M  P  R  E  V  C  I  D  V  G  K  E  F  G  V
-----+-----+-----+-----+-----+-----+-----+
301 CGCGACAACACCTTCTTTAAACCTCCATGTGTGTCCGTCTACAGATGTGGGGTTCCTG
-----+-----+-----+-----+-----+-----+-----+
      A  T  N  T  F  F  K  P  P  C  V  S  V  Y  R  C  G  G  C  C
-----+-----+-----+-----+-----+-----+-----+

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FIG. 2A

1 CGAGCCACGGCTTATGCAAGCAAAGATCTGGAGGAGCACTTACGGTCTGTCCACTGT
 -----+-----+-----+-----+-----+-----+-----+
 61 AGATGA~~ACT~~CACTGACTGTACTCTACCAGATATTGAAATGTACAAGTGTCAAGCTAAG
 -----+-----+-----+-----+-----+-----+-----+
 M T V L Y P E Y W K M Y K C Q L R
 -----+-----+-----+-----+-----+-----+-----+
 121 GAAAGAGGCTGGCAATACAGAGAACAGCCCACTCACTCAAGGACAGAGAGAC
 -----+-----+-----+-----+-----+-----+-----+
 K G G W Q H N R E Q A N L N S R T E E T
 -----+-----+-----+-----+-----+-----+-----+
 181 TATATAATTTCCTGCAGCACATTAATACAGAGATCTTGAAAGTATTGATAATGAGTC
 -----+-----+-----+-----+-----+-----+-----+
 I K F A A A H Y N T E I L K S I D N E W
 -----+-----+-----+-----+-----+-----+-----+
 241 GAGAAAGACTCAATGCATGCCACGGAGGTGTGTATAGATGTGGGAAGAGTTTGAGT
 -----+-----+-----+-----+-----+-----+-----+
 R K T Q C M P R E V C I D V G K E F G V
 -----+-----+-----+-----+-----+-----+-----+
 301 CGCGACAACACCTTCTTTAAACCTCCATGTGTGTCCGTCTACAGATGTGGGGTTCCTG
 -----+-----+-----+-----+-----+-----+-----+
 A T N T F F K P P C V S V Y R C G G C C

FIG. 2A